Controlling Avian Flu and Protecting People's Livelihoods in the Mekong Region

HPAI Research Brief | No. 10 - Year: 2008

Modelling the Temporal and Spatial Dynamics of the Spread of HPAI H5N1 in Northern Viet Nam

P. Walker, S. Cauchemez, R. Metras, D.H. Dung, D. Pfeiffer, and A. Ghani*

Key Findings

- The infectious period appears to have shortened between the second and third waves of HPAI outbreaks in North Viet Nam, perhaps reflecting more rapid reporting and culling.

- There also appears to have been a reduction in commune-level reproductive numbers (R) between the second and third waves.

- Nevertheless, despite vaccination, there remained a substantial number of communes with R>1 that sustained disease transmission during the third epidemic wave.

Highly pathogenic avian influenza threatens the health, livelihoods and income of those reliant on poultry production whilst simultaneously posing serious public health risks, both in terms of the current human mortality and the spectre of a global pandemic. Thus, effective control measures are required to reduce the scope of HPAI outbreaks in poultry, but interventions, which have serious implications for those whom outbreaks already affect the most may result in an unwillingness to report cases, providing the disease with more time and opportunity to spread.

In Viet Nam, based on field experience, the focus of control policies moved from the extensive stamping out, which saw the culling of around 44 million poultry in the first wave of outbreaks, to more focused culling within restricted areas with subsequent outbreak waves in late 2004 and 2005 resulting in the culling of 2.0 and 4.2 million poultry respectively. Beginning in late September and ending in early November 2005, a first mass vaccination campaign covering over 150 million poultry was carried out. Towards the end of this campaign a third wave of outbreaks occurred in North Viet Nam.

Here we describe preliminary results obtained from fitting a spatial transmission dynamics model to this third wave of outbreaks and compare them to those obtained from the second wave of outbreaks beginning in late 2004 which

For more information visit: www.hpai-research.net

preceded the vaccination campaign. The ultimate purpose of the model is to enable *ex-ante* evaluation of HPAI control strategies to inform policy making in Viet Nam, and by extension in other countries in the Mekong region.

Theoretical Background and Data

The likelihood of onwards disease transmission from infected to non-infected communes is determined by two factors: (i) the duration of time the infected commune remains infectious, the infectious period, and (ii) the transmissibility of infection during this period, the reproductive number, i.e. the average number of susceptible communes infected by each infected commune. In the case of Viet Nam, only the dates at which an outbreak within a commune was reported are available. As a consequence, we have attempted to simultaneously estimate the infectious period and the reproductive number for each infected commune.

Figure 1: Spatial and temporal distribution of the second and third wave of HPAI outbreaks in North Viet Nam
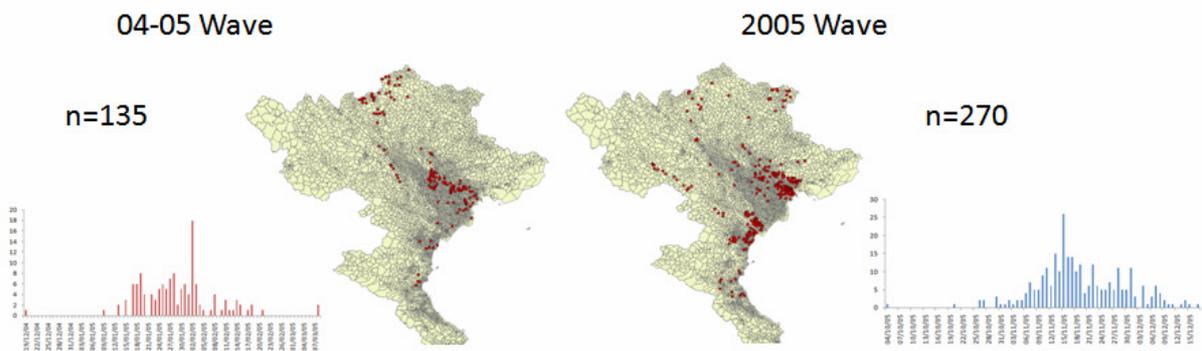

Distribution of Infectious Periods

In the absence of any specific data, we made the strong assumption that, following a report of an outbreak, the poultry within a commune was removed from the outbreak by the end of the following day. We then estimated the infectious period for each infected commune as the time between infection (which is estimated in the model) and the time the outbreak is reported.

Figure 2: Estimated infectious period by calendar time and outbreak wave

2
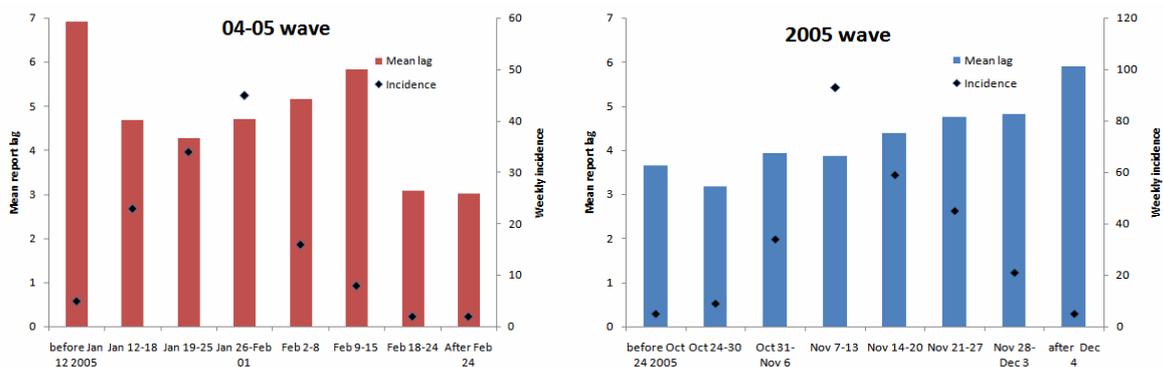
The estimated infectious period appears to increase slightly later on in the 2005 wave of outbreaks (Figure 2). However, during this wave, the infectious period was on average around a day shorter than during the 04-05 wave (Figure 3). In contrast, the long tail in the distribution of infectious periods during the 04-05 wave suggests a situation where, although most outbreaks are reported relatively rapidly, there may have been communes where outbreaks were not reported for a significantly longer period (Figure 3).

Figure 3: Estimated distribution of the infectious period over the complete outbreak for each of the two waves (04-05 and 05)
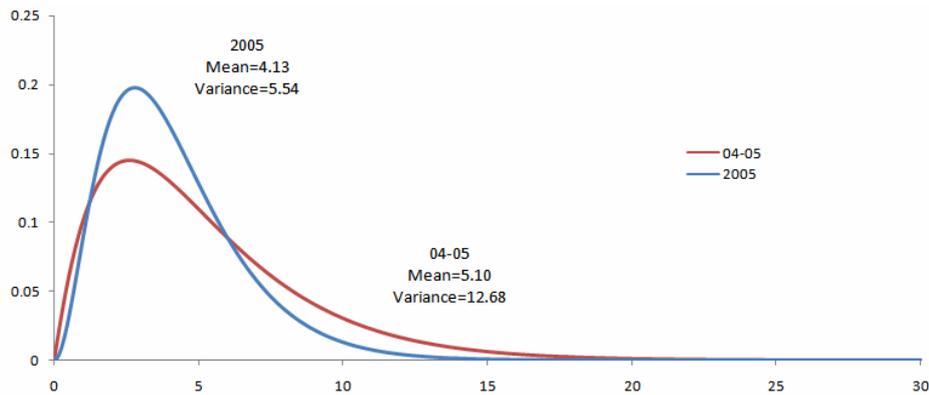
Spatial Transmissibility

To capture the spatial spread of the disease a transmission kernel describing how the probability of transmission is related to the distance from a potential source of infection was fitted.

Figure 4: Daily probability of infection by distance and histogram of expected distance between infection events
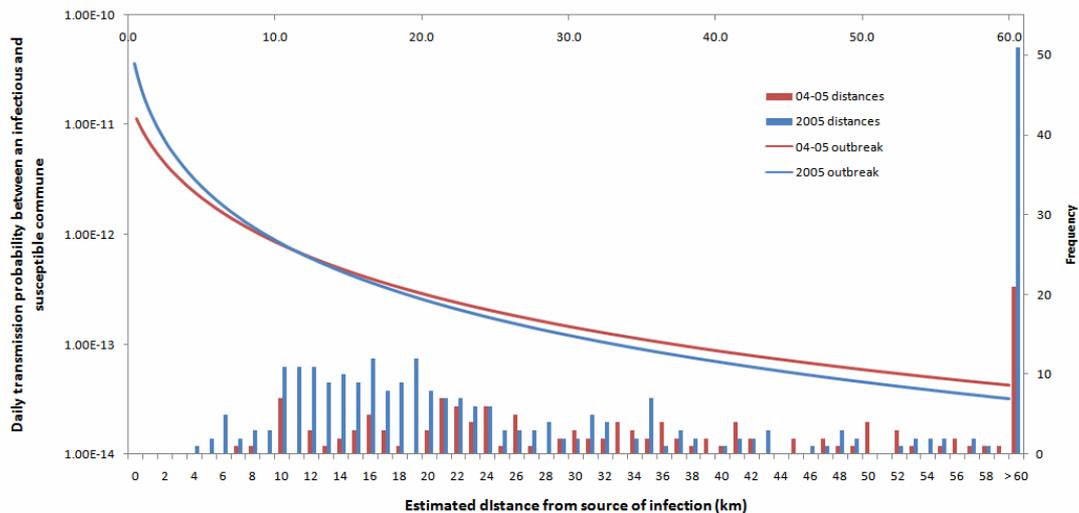

There were no significant differences between the two transmission kernels indicating that there was little change in the underlying spatial transmission process between the two epidemic waves, despite more rapid reporting and vaccination.

3

Local Reproductive Numbers and Risk Maps

Based on the obtained distribution of the infectious periods and the spatial transmission kernel, the local reproductive number for each commune was calculated. This provides the expected number of secondary outbreaks which would have occurred had the first outbreak occurred in a given commune. Commune reproductive numbers were then used to produce risk maps to highlight areas most likely to propagate outbreaks.

Figure 5: Risk maps and local reproductive numbers of the two outbreak waves
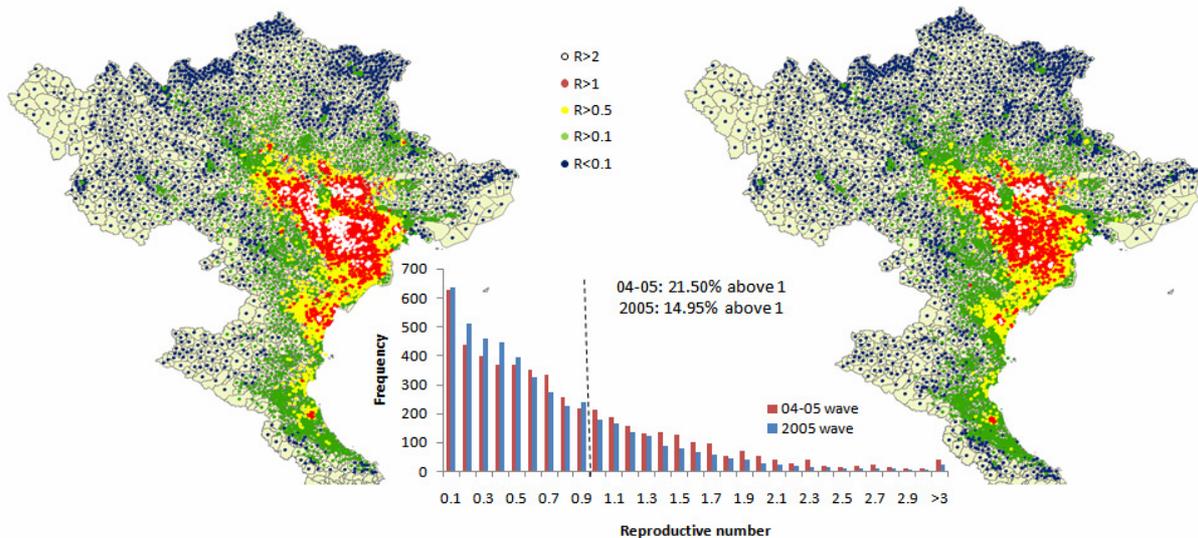
Both risk maps for the 2004-05 and the 2005 wave highlight the Red River delta region as the area of highest risk (Figure 5). The risk map for the 2005 wave of outbreaks contains fewer communes with a reproductive number above the threshold value of 1 needed to generate an epidemic and far fewer with reproductive numbers higher than 2, suggesting that the control measures put in place prior to this outbreak reduced transmission. Both risk maps were unable to reproduce local reproductive numbers which would accurately predict the outbreaks occurring in the Northern provinces near the Northern border suggesting that other factors are driving the epidemic in this region.

Further Work

Further analyses will focus on the outbreaks which have occurred in the South of Viet Nam and, depending upon the availability of the data, the more recent waves of outbreaks since late 2006. Moreover, with more specific data on poultry density, reporting and culling strategies and poultry movements it would be possible to improve the reliability of the results obtained in these preliminary analyses and it may even inform the development of the model in order to capture the elevated risk in areas, such as the Northernmost provinces of Viet Nam, where outbreaks occurred which are not currently captured by the model.

Disclaimer: The views expressed in this paper are solely those of the authors and do not reflect an official position of DFID, MRC, FAO, RVC, IC or RDRC.

*Contact: a.ghani@imperial.ac.uk